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Eclipse Photon and
Electron Algorithms
Reference Guide

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Chapter 9   Dose Optimization Algorithms

General Information about Dose Optimization Algorithms

The dose optimization algorithms used in Eclipse are:

- Photon Optimization algorithm (PO): Determines the optimal field shape and intensity by iteratively conforming the dose distribution to the desired objectives until an optimum solution is reached. Optimizes static field IMRT plans, VMAT (RapidArc) plans, Elekta VMAT plans and Siemens mARC plans based on optimization objectives.
- Dose Volume Optimizer algorithm (DVO): Determines the optimal field shape and intensity by iteratively conforming the dose distribution to the desired objectives until an optimum solution is reached.
- Plan Geometry Optimization algorithm (PGO): Selects the beam angles based on user-defined dose-volume objectives. The PGO algorithm is based on the DVO algorithm and uses the same objectives.
- Progressive Resolution Optimizer algorithm (PRO): Creates VMAT, or RapidArc, plans based on dose-volume objectives.
- Multi-Resolution Dose Calculation algorithm (MRDC): Enables fast dose estimation inside the PO, DVO, PGO and PRO.

Features of Dose Optimization Algorithms

The table is a summary of the features, objectives, parameters and their variants in the dose optimization algorithms. For details, see the corresponding topics.

Table 31   A Summary of the General Features of Dose Optimization Algorithms

	PO	DVO	PGO	PRO
Heterogeneity correction	Yes	Yes	No	Yes
Bolus	Yes	Yes	Yes	Yes
Support devices	Yes	Yes	No	Yes
Dose-volume Objectives	Yes	Yes	Yes	Yes
Mean dose objective	Yes	No	No	Yes

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	PO	DVO	PGO	PRO
Minimum dose	MU objective for VMAT	Min. Fluence	Min. Fluence	MU objective
Normal Tissue Objective	Interactive/Automatic	Static	Static	Interactive/Automatic
Restarting optimization	Yes	Yes (from fluence)	No	Yes
Intermediate dose calculation	Yes	Yes	No	Yes
Output	Fluences for static fields Leaf sequences for VMAT fields	Fluence	Beam geometry	Leaf positions and MU/deg as a function of gantry angle
Geometric optimization	Arc Geometry Tool for VMAT	No	Local/global	Arc Geometry Tool
Dose calculation algorithm	MRDC	MRDC	MRDC	MRDC with progressive dose calculation segments
gEUD objective	Yes	No	No	No
Base dose support	Yes	Yes	Yes	Yes

Bolus and Patient Support Devices

Optimization algorithms take bolus and patient support devices (for example couch structures) into account. They interpret the assigned HU values and handle overlapping structures in the same way as in the dose calculation algorithm. However, because of how AAA and Acuros XB use heterogeneity correction in the full final dose calculation inside bolus and patient support devices, the heterogeneity correction must be turned on in the optimization algorithms. (Information on AAA and Acuros XB: Chapter 4 Photon Beam Source Model on page 35.) If optimization is performed without the heterogeneity correction, the patient support devices are ignored (a warning is given in the calculation log), and bolus are treated as having the density of water.

Note: *The Plan Geometry Optimization (PGO) does not support heterogeneity correction and does not take patient support devices into account.*

Target Masking

The point set for the target is projected to the fluence matrix. Only rays within 0.5 cm from the closest projected point are allowed to have non-zero fluence values. Target masking includes the MLC geometry. This means that any leaf having any points within the 0.5 cm range includes all its rays to the field (in the Y-direction). The field sizes are automatically determined from the masking data.

In the arc optimization algorithms, target masking is used to limit the leaf positions. The target projection may be very different between different gantry angles. While gantry is rotating from one gantry angle to another, the leafs may also be open outside target projection.

Dose Calculation

The dose calculation from the fluences is based on multi-resolution 3D convolution of Monte-Carlo-generated point-spread function kernels (Multi-Resolution Dose Calculation (MRDC) Algorithm on page 185).

For the fluence-based static field IMRT optimization, the dose calculation is straightforward.

The VMAT optimization calculates fluence for dose calculation from a dose calculation segment, in which the MLC configuration and dose rates are converted into a fluence. The fluence models the leakage caused by the rounded leaf ends, tongue-and-groove effect and the transmission through the leafs (Example Sliding Window Case on page 236).

Information on configuring the dose calculation: System Configuration for Dose Optimization on page 208.

Dose-Volume Objectives

The optimization is based on dose-volume objectives (upper and lower objectives defined in the Dose Volume Histogram view inside the Optimization dialog). Dose-volume objectives are used to define the dose as follows:

- *Upper objective*: Used to limit the dose in a given structure (for example, "no more than 20% of the structure may receive more than 25 Gy").
- *Lower objective*: Used to define desired dose levels in target structures (for example, "at least 70% of the structure must receive at least 20 Gy").
- *Upper line objective*: Used to limit the dose in a given structure for all volume levels.

If the dose-volume objectives are not met, a weighted quadratic cost is added to the total objective function. For the upper objective, the cost is applied for the portion of doses that exceed the desired dose value and volume level. For the lower objective, the cost is applied for the portion of doses that fall short of the desired dose value and volume level. For example:

Equation 51

$$\text{costD}=\text{w}\times(\text{D-D}_{\text{target}})^2$$

where

D	=	Dose
w	=	Weight

The dose-volume objective of each point introduces discontinuities in the optimization space, and each additional objective may create thousands of new local minima. To overcome this, the DVO and PRO also have a more powerful dose-volume objective form, the line dose-volume objective, that allows using very complex and expressive dose-volume objectives while creating fewer local minima. The PO supports optimization of line objectives, but not creation of new ones.

Smoothing Objectives

The fluence needs to be smooth to enable leaf motion calculations with the LMC. Fluence smoothness is ensured by adding an objective that includes the difference between the neighboring fluence values (X smooth and Y smooth). This objective is linear up to the value of 3% of the maximum fluence value, where it saturates to a constant value. The saturation non-linearity allows for large fluctuations in the fluence where required. The smoothing is performed in both X and Y-directions of the fluence, with different user-configurable weightings. Typically, it is more important to have a smoother fluence in the X-direction to ensure the minimal MU factor for the LMC.

Smoothing objective is available only for static field IMRT optimization with DVO and PO.

MU Objective

The MU Objective can be used to control the number of MU that the PO or PRO optimizer produces. Minimum and maximum values can be defined. An extra multiplier is applied to the total objective function value if the number of MU is not in the desired range. Strength value can be used to modify the strength of the effect. Because the value is a multiplier to total objective function value, the relative effect of the MU objective remains the same even when the priorities of the dose-volume objectives are changed.

Normal Tissue Objective

The Normal Tissue Objective is used for the part of the body which does not include the PTV to limit the dose level and prevent hot spots in healthy tissue. In addition, the Normal Tissue Objective can be used for obtaining a sharp dose gradient around the PTV.

Note: *With the PO and PRO algorithms you can also use the automatic Normal Tissue Objective (Automatic Normal Tissue Objective in PO and PRO on page 183).*

Normal Tissue Objective Shape

The shape of the Normal Tissue Objective is controlled with the following parameters:

- Distance from PTV border (X_{start})
- Start dose (f_0)
- End dose (f_∞)
- Fall-off (k)

The shape of the Normal Tissue Objective ($f(x)$) as a function of the distance from PTV border (l) is calculated as:

Equation 52

$$f(x) = \begin{cases} f_0 e^{-k(x-x\text{start})} + f_\infty\left(1 - e^{-k(x-x\text{start})}\right), & x \geq x_{start} \\ f_0, & x < x_{start} \end{cases}$$

The figure shows a typical shape of the Normal Tissue Objective.
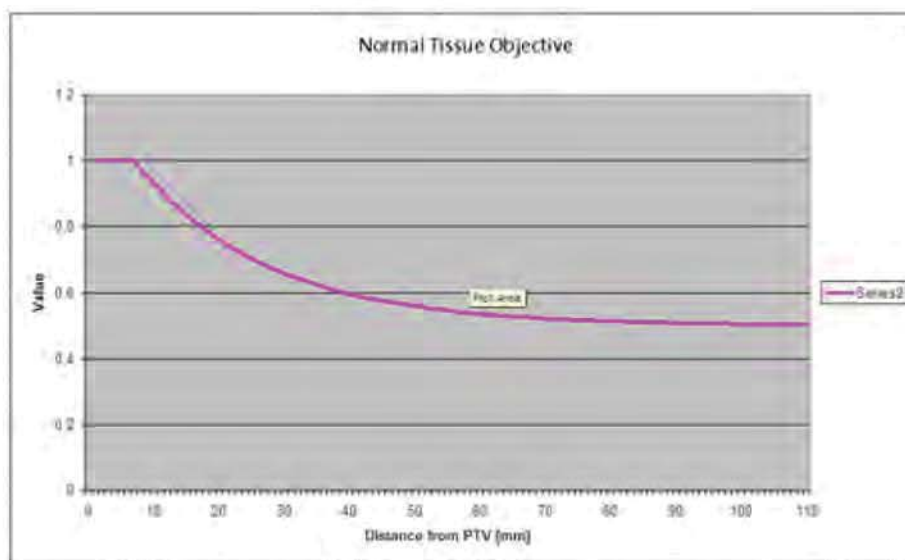
Figure 30   Example Shape of the Normal Tissue Objective

The shape of the Normal Tissue Objective presented in the figure has been calculated with the following parameter values:

- X_{start} = 10 mm
- f_0 = 1.1
- f_∞ = 0.5
- k = 0.05

Normalization of the Normal Tissue Objective is done as follows: level 1.0 (100%) corresponds to the lowest upper objective defined for the target. If no upper objective is defined, level 1.0 (100%) is 1.05 times the highest lower objective defined.

In addition to the parameters that control the shape of the Normal Tissue Objective, the importance of the Normal Tissue Objective in relation to the other optimization objectives is controlled with the Priority parameter. The Normal Tissue Objective is taken into use by defining a value for the Priority parameter. Then the Normal Tissue Objective values are calculated for all body points. If there are several PTVs, the Normal Tissue Objective value for a specific body point is the highest one of the Normal Tissue Objective values calculated at this point for all the PTVs. If the value of the Priority parameter is set to zero, the optimization does not use the Normal Tissue Objective.

Note: *Any structure with at least one lower objective is considered a PTV by the Normal Tissue Objective.*

Normal Tissue Objective Parameters

The table shows the Normal Tissue Objective parameters and their default values.

Table 32   Default Values for the Normal Tissue Objective

Parameter name	Range	Default	Use of Parameter
Distance from PTV/ target border [cm]	-20–20	1.0	Determines the area where the Normal Tissue Objective value must be constant. Expressed in centimeters.
Start dose [%]	0–1000	105	Determines the relative dose level in the Normal Tissue Objective at the PTV border. Expressed in percentage.
End dose [%]	0–1000	60	Determines the relative dose level in the Normal Tissue Objective in the area furthest from the PTV border. Expressed in percentage.
Fall-off	0–100	0.05	Determines the steepness of the Normal Tissue Objective curve shape.
Priority	0–1000	0	Determines the relative importance of the Normal Tissue Objective. To use the Normal Tissue Objective in optimization, the Priority parameter must have a non-zero value.

Automatic Normal Tissue Objective in PO and PRO

The Automatic Normal Tissue Objective uses a set of internal parameters, so the parameters in the Normal Tissue Objectives dialog box have no effect on it. The internal parameters depend on the distances of the high dose areas from the target, and they are adapted dynamically so that they are suitable for the patient anatomy and the objectives during the optimization. The Automatic Normal Tissue Objective monitors the area within a certain distance around the target, and if there are doses that are exceptionally high considering the distance from the target, it tries to reduce the dose at the area using the user-defined priority value.
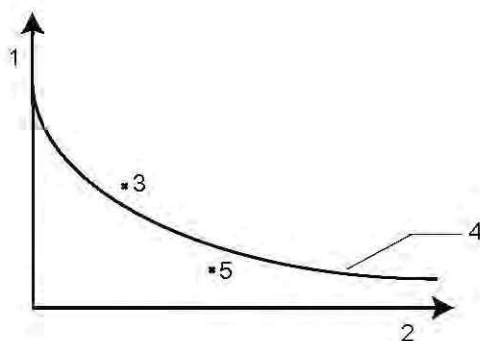
1. Dose
2. Distance from the target
3. The dose at this point is above the accepted dose level, and therefore the optimization tries to reduce the dose in this area.
4. Accepted dose level for this case.
5. Points within this region are not affected.

Figure 31   Adjustment Criteria for Automatic Normal Tissue Objective

Automatic Normal Tissue Objective tries to reduce doses the same way as Normal Tissue Objective, but the key difference is that the accepted dose level curve (4 in the above figure. See also: Figure 30 on page 182) is not defined by the user, but calculated automatically.

Volume Representation in DVO, PGO and PRO

Volumes are represented by point clouds generated from user-defined segments. The sampling density of the point clouds is determined by the resolution and shape of the user-defined segments. Sub-volumes located close to the surface of the structures are represented more accurately, and the user-defined resolution is used inside the volume. If the Normal Tissue Objective (NTO) is used, additional points are used near target boundary to increase the accuracy (Normal Tissue Objective on page 181).

Both the representation accuracy of volumes and the total number of points affect the memory consumption and speed of the optimization algorithms. Using high numbers of points helps to achieve higher accuracy in the volume representation, however, it will also increase memory consumption. Reducing the number of points will decrease memory consumption, but it may affect the accuracy of the volume representation adversely and compromise the quality of the DVH shown in the optimization. The optimization algorithms have the following restrictions related to the volume representation:

- DVO algorithm: Does not restrict the total number of points.
- PGO algorithm: Estimates the memory consumption at the beginning of the optimization. If the memory does not suffice for the optimization, an error message is shown, instructing the user to decrease either the number of points or initial fields in the plan.
- PRO algorithm: Does not restrict the total number of points.

Information on volume representation in PO: Photon Optimization Algorithm (PO) on page 186.

Minimal Fluence Objective in DVO and PGO Optimization

An additional objective is provided for the definition of the required minimal fluence (minimize dose defined in the Optimization dialog box). The minimal fluence objective works on per field basis. The optimization does not value extra fluence outside the target if no critical organs have been defined there. The minimal fluence objective allows for natural minimization of the fluence without introducing additional (or even artificial) critical organs.

Multi-Resolution Dose Calculation (MRDC) Algorithm

The Multi-Resolution Dose Calculation (MRDC) algorithm is used for fast dose estimation inside the PO, DVO, PRO and PGO algorithms. The high speed of the MRDC algorithm allows the optimization algorithms to perform full dose computation during each iteration.

The MRDC algorithm is based on the convolution superposition principle, and it uses 3D convolution scatter computation.

The scatter model is based on 3D superposition of point spread functions in the patient model. The point spread functions are built from Monte Carlo calculations.

Multi-resolution scatter computation calculates the scatter component using variable resolutions. Finer resolution is used close to the location of the primary interaction, while much lower resolution is used to compute the scatter component for larger distances (as far as 25 cm from the primary interaction). The convolution uses the divergence-corrected single kernel model in water-equivalent material.

Energy Spectrum

The energy spectra are based on the Monte Carlo calculations[37]. The nominal energy is used to select a spectrum from a set of precalculated data. The spectrum affects the primary component function and the point spread function. The primary component is corrected for inhomogeneities. This precalculated spectrum can be slightly optimized during the configuration of the PO, DVO or PRO algorithm in Beam Configuration.

Intensity Profile

The intensity model of the primary component is radially symmetric around the central axis. The intensity profile is optimized from the measurement data. Diagonal profile measurements may improve the accuracy of MRDC for large field sizes.

Electron Contamination

The MRDC algorithm models the electrons created in air and the secondary collimators between the photon source and the body. Electron contamination is modeled as a depth-dependent intensity curve and a fluence-dependent spreading of contamination electrons, also extended outside the field area. The shape and the amplitude of the electron contamination curve are optimized during the configuration of the optimization algorithm.

Modeling of the Second Source

Radiation emerging outside the linac target (for instance, from the flattening filter) is modeled in the MRDC algorithm as a second photon source. The SSD of the second source, spreading of the second source photon fluence, effective photon energy, and the second source amplitude relative to the primary source are optimized during the configuration of the algorithm.

Photon Optimization Algorithm (PO)

The Photon Optimization algorithm (PO) optimizes static field IMRT plans, VMAT plans (RapidArc and Elekta VMAT) and Siemens mARC plans.

The PO combines the previous optimization methods used for static field IMRT and arc field IMRT with DVO and PRO.

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[37] Mohan et al. Energy and angular distributions of photons from medical linear accelerators. Med. Phys. 12 (5), Sep/Oct 1985.

The main difference of the PO algorithm from the earlier optimization algorithms (DVO and PRO) is that the earlier optimization algorithms used a point cloud model for defining structures. The PO algorithm uses a new structure model, where structures, DVH calculation and dose sampling are defined spatially by using one single matrix over the image.

The voxel resolution of the matrix is using fixed values of 1.25 mm, 2.5 mm or 5 mm. This resolution defines the planar X and Y resolution in the slices. The Z resolution orthogonal to the slices is a function of chosen resolution and the slice spacing. For example, if the original image has a slice resolution of 1 mm × 1 mm and a slice spacing of 8 mm and the user has defined the optimization resolution to be 2.5 mm, then the optimizer uses the matrix of 2.5 mm × 2.5 mm × 4 mm.

This matrix defines the locations of the structures and the sampling of the dose, and it substitutes the previously used point clouds.

The figure illustrates a structure segment sent from the client, the image slices and the dose matrix samples (stars) that define the voxels that represent the structure inside the optimizer. These samples also represent the places where the total dose from each field is evaluated.
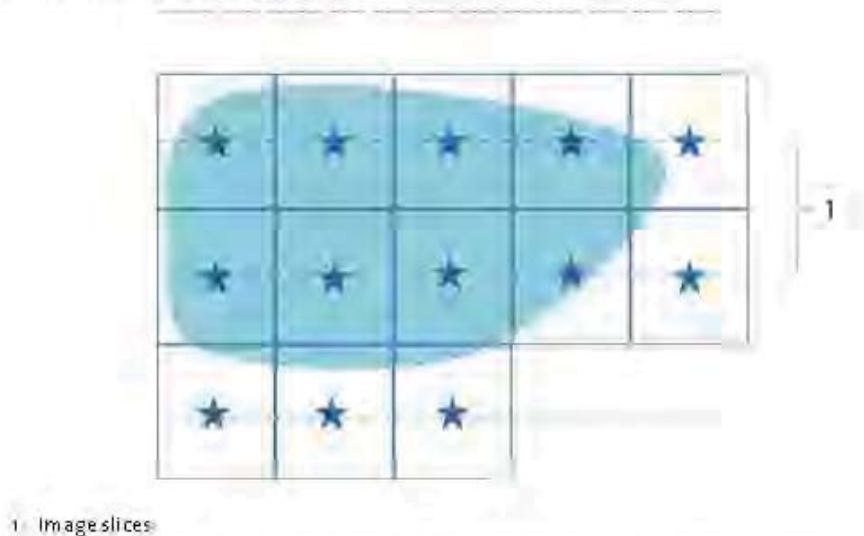

1   Image slices

Figure 32   Structure Model in Photon Optimization Algorithm

The DVH for the structure is evaluated using volume weights defined for each voxel. The volume weight of the voxel defines the ratio of the original structure segment inside the voxel. For small structures, the DVH is super-sampled from the dose matrix to make the DVH look smoother.

In order to minimize the run time memory consumption, the matrix size is first set to the size of body bounding box. Then the field field-of-views are formed, and the final matrix size is set to contain only the part of the body bounding box that can receive radiation from the fields.

Photon Optimization Algorithm and IMRT

For IMRT, the PO determines the optimal field shape and intensity by iteratively conforming the dose distribution to the desired objectives until an optimum solution is reached.

For each field, the PO fits the fluence to the target projection with 5 mm margin. Then the created fluence object is expanded symmetrical to the field isocenter (by adding fluence pixels with 0 value). The maximum size of the fluence object is 40×40 cm. The size of the fluence object determines the region where the user can edit the fluence.

The PO performs the optimization for an IMRT plan as a minimization problem using simple gradient optimization with line minimization. Initially, all the fluences are zero, or, alternatively, the fluences from a previous optimization can be used as the initial guess. The optimization modifies these fluences in each iteration and calculates the dose from the fluences after each modification.

Once the doses at the points of the point clouds representing the patient volumes are evaluated, the objectives at the points and the derivatives of the point objectives can be calculated. The cost functionals are evaluated for each point in each volume. The derivatives of the costs at each point are back-projected to the fluences, forming the gradient.

The PO uses the gradient search method. The gradient search is divided into two phases; gradient evaluation and line search. Gradient evaluation generates the gradient direction and the gradient length, and line search evaluates the objectives on a line segment along the gradient and finds the minimum along the line segment.

The PO can use a calculated plan dose as an intermediate dose when optimizing an IMRT plan. The algorithm calculates the difference between the intermediate dose and the first round optimization result and uses this difference to compensate the optimization result in the consequent iterations. If a new intermediate dose is calculated after the first optimization iteration, the difference is calculated again and it will be used to compensate subsequent iterations. Using an intermediate dose is particularly useful if the DVH calculated during optimization deviates from the DVH produced during dose calculation, for example when there is a lot of heterogeneity in the volume to be treated.

Photon Optimization Algorithm and VMAT

The PO creates VMAT (RapidArc, Elekta VMAT, Siemens mARC) plans based on dose-volume objectives. VMAT fields use DMLC, variable dose rate and variable gantry speeds.

The PO algorithm generates a sequence of control points which define MLC leaf positions and MU/deg as a function of gantry angle. MU/deg is encoded in DICOM and the Varian system database with the cumulative meterset weight, which defines the increase in MU between control points relative to the total MU in the field. This information is transferred to the treatment machine as such, and the machine control system determines how dose rate and gantry speed will be modulated to deliver the plan. After dose is calculated, Eclipse shows estimated dose rate and gantry speed values in the Field Properties and MLC Properties pages. These estimates are not part of the information sent to the treatment machine.

The PO algorithm uses an objective function to optimize the plan and to evaluate its quality. The objective function is the sum of the dose-volume and other user-defined objectives.

Progressive Resolution

The initial conditions for the PO algorithm are defined using control points to represent each VMAT field. The algorithm uses multi-resolution approach (first described in the research on volumetric modulated arc therapy[38]) to optimize the plan. This means that the dose is modeled using first a lower number of dose calculation segments that are distributed evenly in each field. The number of dose calculation segments increases when moving from one multi-resolution level to another.

The dose in a dose calculation segment is calculated from the combined fluence through the MLC apertures at the control points located within a certain sector of the arc. Leaf motion is modeled by interpolating leaf positions between the control points. Leaf tongues are modeled by modifying the MLC aperture outline to effectively account for the tongue-and-groove effect.

The angle resolution of the dose calculation segments gets more accurate as the optimization progresses, and in consequence, the dose also gets more accurate. The number of control points remains the same during the whole optimization.

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[38] Otto, K: Volumetric Modulated Arc Therapy: IMRT in a Single Arc, Medical Physics, Vol. 35, no. 1, 2008, 310–317.

At the beginning of the optimization, the initial MLC shapes are conformed to the targets and the initial dose rates are equal for all dose calculation segments. The MLC shapes and dose rates of the different control points in the VMAT field are optimized. During the initial phases of the optimization bigger adjustments are made in leaf sequencing. The size of these adjustments decreases as the optimization progresses through the levels.

During the optimization, the algorithm proceeds through multi-resolution levels progressively increasing the accuracy of the dose calculation. At the first multi-resolution level, only a few dose calculation segments are used to model the dose, and each multi-resolution level contains progressively more dose calculation segments. The angle between the resulting dose calculation segments on the last multi-resolution level (4) will be approximately 2°-4°.The total number of dose calculation segments used depends on the span of the arc.

Inside each multi-resolution level there are several steps. Each step has its own internal calculation parameter set. The optimization allows some discontinuities in the delivery during early phases of the optimization, and decreases the size of the discontinuities stepwise as the optimization progresses. At the step borders, the delivery is forced to be within specified discontinuity levels. This may increase the objective function values when moving from one step to the next, and a peak in the objective function curve may be seen. The number of steps in different multi-resolution levels varies. Due to the nature of the optimization process, the PO algorithm is not fully deterministic. Therefore successive optimizations with the same constraints may yield different results.

Avoidance Sectors for VMAT

Avoidance sectors are ranges of gantry rotation with a zero delivered dose rate. You can define up to two avoidance sectors for each arc field in the optimization. The minimum length for an avoidance sector is 15 degrees. Similarly, the minimum length for the beam-on sector between two avoidance sectors, or between gantry start/stop angles and an avoidance sector is 15 degrees.

Avoidance sectors are supported for Varian treatment units and for Siemens mARC.

Jaw Tracking for VMAT

Jaw tracking dynamically moves the collimator jaws during beam-on to keep them as close to the actual MLC aperture as possible. This reduces leakage between the MLC leaves. The initial user-defined collimator jaw positions for the plan are used as the maximum limit for the jaws. Jaw tracking does not move the collimator jaws outside this maximum limit. Collimator jaws can follow the MLC aperture inside the target projection, if necessary.

Note: *Not all VMAT-capable Varian linear accelerators support jaw tracking. The option can be selected in optimization only for plans to be delivered with a treatment machine that supports jaw tracking. Jaw tracking is automatically on for Elekta MLCi and MLCi2.*

PO supports jaw tracking via the motion modes and speed limits that are defined in RT Administration for each collimator (IEC X1, X2, Y1, Y2). Motion modes must be the same for both jaws on the axis. Collimator motion modes override the Field X setting earlier used for jaw tracking.

The collimator motion mode in RT Administration can have the following values:

- Empty: Not allowed if jaw tracking is requested.
- Static: Collimator does not move during the arc delivery.
- Dynamic: Collimator moves within the set maximum speed limit during the arc delivery.
- Pseudo (also known as non-existent or virtual jaw); A static position is determined for the collimator within the initial field size based on the projection of the target structure(s) during pre-processing. There is a maximum leaf transmission value (1%) for using the Pseudo mode. Speed limits are ignored. Post-processing may re-position the collimators according to validation rules specific to the treatment unit model.
- Multiple Static Positions: Collimator can move obeying the set speed limit, but only between control points where the beam is off. The initial field size is used as a maximum opening limit.

Biological gEUD Objectives

The PO supports three new objective types for biological optimization using generalized Equivalent Uniform Dose (gEUD) formalism: lower gEUD, upper gEUD and the target gEUD constraint. For each objective, the user defines a target gEUD value, biological parameter a and objective priority w. Optimization then evaluates the gEUD(a) values for the structure, and a square law cost is applied when an objective is not met in the same manner as in normal dose-volume objectives:

Equation 53

$$\mathrm{cost}(gEUD(a)) = W \times (gEUD(a) - EUD)^2$$

where

cost (gEUD)   =   Square law cost

a =   Biological parameter controlling the dose distribution inside the structure. Typical values range from −40 to +40.

| W | = | Priority. |
| EUD | = | Target value for EUD. |

The above equation describes the target gEUD constraint. For the lower gEUD constraint, the cost is 0 when $gEUD(a) > EUD$. For the upper gEUD constraint, the cost is 0 when $gEUD(a) < EUD$.

$gEUD(a)$ is defined as:

Equation 54

$$gEUD(a) = \left(\frac{1}{V} \times \sum_{v} D(x)^a \right)^{\frac{1}{a}}$$

where

a	=	Biological parameter controlling the dose distribution inside the structure. Typical values range from −40 to +40.
V	=	Volume/Structure.
D	=	Dose in position x inside the volume V.

Mean Dose Objective

Mean dose objective is used to define the mean dose that should not be exceeded for a structure. The objective defines the mean dose in Gy, but does not define any percentage of the structure volume that should not receive more than this dose. Mean dose objective is visualized in DVH during optimization, and it can be adjusted interactively during optimization. Mean dose objective cannot be used to increase the dose to a structure.

Intermediate Dose

The existing dose can be used as an intermediate dose when continuing the optimization. This can be done manually by restarting the optimization and selecting the option to use the current plan dose as an intermediate dose for optimization, or automatically by selecting "Automatic intermediate dose" in the Optimization dialog box when optimizing for the first time. This is useful especially if the DVH calculated during arc optimization deviates from the DVH produced during dose calculation, for example when there is a lot of heterogeneity in the volume to be treated.

The optimization algorithm can adjust the leaf sequences for VMAT fields, or fluences for static IMRT field based on the intermediate dose. It calculates the error between the first round optimization result and the dose calculation, and during the second optimization round, when the optimization is finalized, it compensates for the differences and tries to achieve a better agreement. For VMAT, the second optimization round starts at the last multi-resolution level (level 4).

Restarting Optimization

VMAT optimization can be restarted from user-defined arc fields. The user-defined fields may be produced, for example, in a previous arc optimization, or they may be created manually.

Before restarting the VMAT optimization, the algorithm re-samples the arc treatment to suitable control point spacing. The optimization restarts from the last multi-resolution level that has the most accurate dose modeling. To allow bigger adjustments to the leaf sequence, the user should rewind the multi-resolution levels. However, the dose on the earlier multi-resolution levels, calculated with the MRDC algorithm, is less accurate.

If the arc field does not contain a DMLC, VMAT optimization is started from the first multi-resolution level.

In IMRT optimization, initially all the fluences are zero, or, alternatively, the fluences from a previous optimization can be used as the initial guess. The IMRT optimization modifies these fluences in each iteration and calculates the dose from the fluences after each modification.

Calculation Options for the PO Algorithm

The PO algorithm has the following calculation options:
- Inhomogeneity correction: Defines whether tissue heterogeneity correction is applied during optimization.
- Air cavity correction: An additional parameter for fine-tuning inhomogeneity correction. This parameter has no effect if the Inhomogeneity correction parameter is set to Off. When the air cavity correction option is used, the dose in an air cavity is smaller than without this option. On the other hand, the target/any part of the target should not be contoured in air, as the target will not get enough dose.

Additionally, the following options are available for static IMRT fields:
- Smooth X: Smoothing of the field fluence on X axis.
- Smooth Y: Smoothing of the field fluence on Y axis.

Dose Volume Optimizer (DVO) Algorithm

Eclipse IMRT is capable of creating highly conformal dose distributions by optimizing the beam intensity modulation from user-defined dose volume objectives. The algorithm used in Eclipse IMRT, Dose Volume Optimizer (DVO), determines the optimal field shape and intensity by iteratively conforming the dose distribution to the desired objectives until an optimum solution is reached.

For each field, the DVO fits the fluence to the target projection with 5 mm margin. Then the created fluence object is expanded symmetrical to the field isocenter (by adding fluence pixels with 0 value). The maximum size of the fluence object is 40×40 cm. The size of the fluence object determines the region where the user can edit the fluence.

The dose optimization algorithm performs the optimization as a minimization problem using simple gradient optimization with line minimization. Initially, all the fluences are zero, or, alternatively, the fluences from a previous optimization can be used as the initial guess. The optimization modifies these fluences in each iteration and calculates the dose from the fluences after each modification.

Once the doses at the points of the point clouds representing the patient volumes are evaluated, the objectives at the points and the derivatives of the point objectives can be calculated. The cost functionals are evaluated for each point in each volume. The derivatives of the costs at each point are back-projected to the fluences, forming the gradient.

The optimization uses the gradient search method. The gradient search is divided into two phases; gradient evaluation and line search. Gradient evaluation generates the gradient direction and the gradient length, and line search evaluates the objectives on a line segment along the gradient and finds the minimum along the line segment.

The DVO algorithm can use a calculated plan dose as an intermediate dose when optimizing a plan. The DVO algorithm calculates the difference between the intermediate dose and the first round optimization result and uses this difference to compensate the optimization result in the consequent iterations. If a new intermediate dose is calculated after the first optimization iteration, the difference is calculated again and it will be used to compensate subsequent iterations. Using an intermediate dose is particularly useful if the DVH calculated during optimization deviates from the DVH produced during dose calculation, for example when there is a lot of heterogeneity in the volume to be treated.

Plan Geometry Optimization (PGO) Algorithm

The Plan Geometry Optimization (PGO) algorithm enables the Eclipse Beam Angle Optimization, an integrated optimization option for the Eclipse treatment planning system, and is an essential component of effective intensity-modulated radiotherapy (IMRT). Beam Angle Optimization is an automated tool for selecting the suitable beam angles based on user-defined dose-volume objectives that speeds up the planning process for IMRT treatments. Beam Angle Optimization is performed with the PGO algorithm, which is based on the Eclipse DVO algorithm. Plan Geometry Optimization is designed to be run prior to Dose-Volume Optimization. The same DVH-based objectives can be used in both optimizations.

Global Optimization Mode for Plan Geometry

Global optimization creates the new field geometry, which can be either coplanar or non-coplanar, depending on user-defined optimization parameters. The optimization starts from a set of uniformly distributed fields, and then narrows the number of fields down to a set that best fulfils the optimization objectives defined for the patient structures.

The global optimization mode starts with a large initial number of fields either in a 2D or 3D geometry. The PGO uses a fixed isocenter, which means that all fields in the initial field distribution share the same isocenter copied from the first field present in the plan before the PGO is started.

This is done by first optimizing a few fluences and removing fields individually in each iteration. The effect of this removal is evaluated by calculating the corresponding objective function value. The fields whose removal causes the smallest increase in the value of the objective function can be considered less important and are removed from the field geometry. The iterations are continued until the desired number of fields for the final plan has been reached. You can control the number of fields to be excluded after each iteration with a parameter value.

Initial Field Geometries

The way new fields are created depends on the selected global optimization mode. The optimization mode is defined with the *Initial field distribution* parameter. The global optimization mode can be one of the following:

- Coplanar (2D) field geometry: Creates equally spaced fields by increasing the gantry values. The couch angle is always zero (in IEC 61217 scale, which corresponds to 180 degrees in the Varian standard scale).

- Non-coplanar (3D) geometry: Creates fields by uniformly positioning them in three-dimensional space. The angle of each field to its closest neighbor is approximately the same for all fields. Opposing fields are avoided.

> **Note:** *Both the global and local optimization modes exclude fields that enter the patient through the end(s) of the CT stack.*

The initial number of fields in both geometries is controlled with a parameter. The maximum initial number of fields is 400.

You can also specify a limit for the collimator angle between adjacent fields. If the limit is set to zero, the collimators are kept at zero angle. If the limit is set to 180 degrees, the direction of the MLC leaves coincides with the shortest dimension of the PTV in the BEV.

You can also control the offset for the gantry angles in the coplanar field geometry with the *Coplanar offset angle* parameter. This parameter does not affect the non-coplanar initial field distribution.

In the non-coplanar field geometry, you can enter a limit for the elevation angle of the fields from the coplanar plane. The fields in the initial field distribution do not have elevation angle values higher than the specified limit.

Complete list of optimization parameters: Input Parameters for PGO on page 216.

Removing Forbidden Fields from the Initial Field Distribution

The initial field distribution may contain fields that cannot be used for dose calculations. Some fields might also be impossible to deliver due to the physical characteristics of the treatment unit (some gantry and/or couch rotations may not be feasible for the treatment unit). To perform plan geometry optimization only for valid fields, the following fields are excluded from the initial field distribution:

- Fields intersecting the end(s) of the CT stack

    The field geometry in the initial field distribution is checked for fields entering the patient through the ends of the CT stack. If found, such fields are removed.

- Fields with forbidden gantry/couch angle combinations

    The PGO reads the forbidden gantry/couch angle combinations from the GantryCouchAngleCombinations.txt file from the beam data directory root. If this file is not found in the PGO directory, it is created automatically. You can edit this file to include individual specifications for forbidden gantry/couch angle combinations.

The format of the GantryCouchAngleCombinations.txt file is the following:

[n]   [m]

[t1]		[t2]	...	[tm]
[g1]	0/1	0/1	...	0/1
[g2]	0/1	0/1	...	0/1
...				
[gn]	0/1	0/1	...	

where

n	=	Number of limits for gantry angle
m	=	Number of limits for couch angle
g1	=	First limit for gantry angles
gn	=	Last limit for gantry angles
t1	=	First limit for couch angles
tm	=	Last limit for couch angles
0	=	Forbidden gantry/couch angle combination
1	=	Allowed gantry/couch angle combination

The following shows an example of the GantryCouchAngleCombinations.txt file.

Table 33   Example Forbidden Gantry/Couch Angle Combinations file

36		36											
	0	10	20	30	40	50	60	70	80	...	330	340	350
0	1	1	1	1	1	1	1	1	1	...	1	1	1
10	1	1	1	1	1	1	1	1	1	...	1	1	1
20	1	1	1	1	1	1	1	1	1	...	1	1	1
30	1	1	1	1	1	1	1	1	1	...	1	1	1
40	1	1	1	1	1	1	1	1	1	...	1	1	1
50	1	1	1	1	1	1	1	1	1	...	1	1	1
60	1	1	1	1	1	1	1	1	1	...	1	1	1
70	1	1	1	1	1	1	1	1	1	...	1	1	1
80	1	1	1	1	1	1	1	1	1	...	1	1	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...
330	1	1	1	1	1	1	1	1	1	...	1	1	1
340	1	1	1	1	1	1	1	1	1	...	1	1	1
350	1	1	1	1	1	1	1	1	1	...	1	1	1

In an automatically created gantry/couch angle combinations file, the limits for gantry and couch angles are specified with 10-degree intervals. Additional ranges for the limiting angles can be entered in, for example, MS Excel.

Note: *The number of specified gantry limits must be equal to n, and the number of specified couch limits equal to m; otherwise the PGO cannot read the gantry/couch angle combinations file.*

Final Number of Fields in the Plan

The final number of fields left in the treatment plan after the global optimization is controlled with the following parameters:

- Minimum number of fields: If this value equals the maximum number of fields, the specified number of fields is left in the final plan
- Maximum number of fields: If this value exceeds the Minimum number of fields, the final field geometry has an optimal number of fields which belongs to the specified range.

The optimal number of fields is determined from the value of the objective function as follows: if the value of the objective function increases because of the removal of fields, the removal is canceled and the value of the field reduction rate is reduced to one half of the original value. Then the optimization iteration is re-calculated with the reduced field reduction rate. This is continued until the

- Decreased value of the objective function is obtained, and fields are removed according to the current field reduction rate, or
- Removal of the fields is canceled and the global optimization stops.

The effect of the number of fields on the objective function is adjusted with the field number objective (Field Number Objective on page 199).

Number of IMRT Iterations

The number of IMRT iterations run during one PGO iteration in the global optimization mode is controlled with a parameter value. It is recommended to use the minimum value of 3 for this parameter.

Field Reduction

The number of fields to be removed at the end of a global optimization iteration is controlled with the Field reduction rate (FRR) parameter. The number of fields to be removed is calculated as:

Equation 55
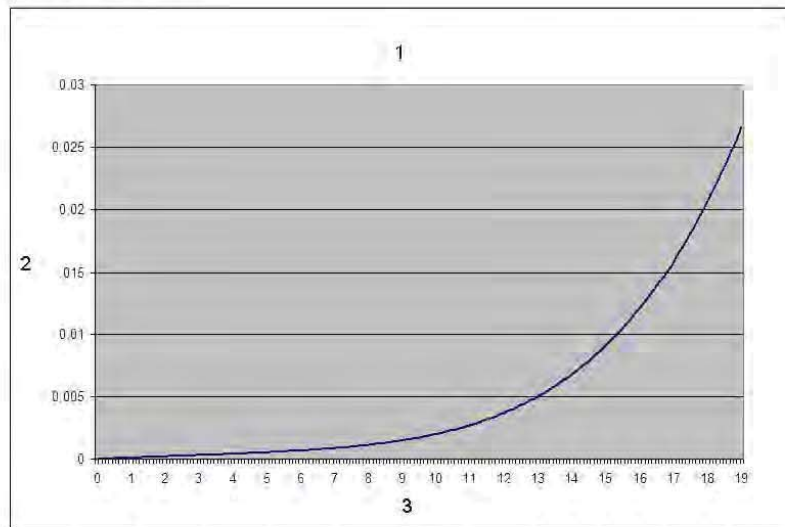
$$n_{removed} = FRR \times (n_{left} - n_{min})$$

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where

$n_{removed}$	=	number of fields to be removed
n_{left}	=	number of fields which are currently included in the plan
n_{min}	=	minimum number of fields to be left in the final plan

As a result, global optimization aims at leaving n_{min} fields in the plan.

Field Number Objective

1. Field number objective
2. Constraint value
3. Number of fields in the plan

Figure 33   Shape of the Field Number Objective

With the Field Number objective, the number of fields in the final plan is typically limited to fewer than 10 fields. The strength of the objective is adjusted with a weight parameter.

Lateral Inhibition

To prevent the PGO from removing all fields entering from a bad direction during the first global optimization iterations, the algorithm performs a lateral inhibition calculation. Lateral inhibition enhances the values of the objective function close to removed fields. The inhibition gives increased objective function values to fields located close to removed fields, which results in retaining these fields in the plan. The calculation of the lateral inhibition is cumulated in the values of the objective function within one iteration. The effect of lateral inhibition is reset when the next iteration starts. The shape of the lateral inhibition function (LI) is a linear combination of cosine powers:
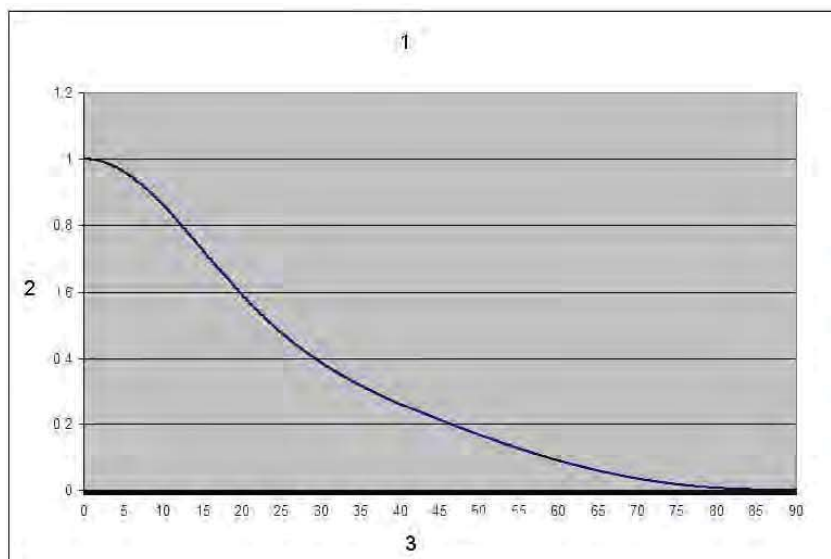
Equation 56

$$LI = C \times (\cos^{2.5}\alpha + \cos^{18}\alpha) \times std$$

where

C	=	value of the weight parameter to control the strength of the lateral inhibition
α	=	angle to the removed field
std	=	standard deviation of the field removal effects

The shape of the lateral inhibition function with std = 1 is shown in the figure.

1. Lateral inhibition
2. Function value
3. Angle to the removed field

Figure 34   Shape of the Lateral Inhibition Function

The values of the objective function (OF) are then updated with the lateral inhibition as:

Equation 57

$$OF_{new}=OF_{old}+LI$$

Thus, the importance of fields located close to a removed field is increased in relation to the remaining fields.

Proximity Effect

Sometimes the PGO results in plans containing fields located close to each other. In a final treatment plan, this is usually considered undesirable, because it can easily produce hot spots in normal tissue. To avoid closely located fields in the final treatment plan, the PGO performs a proximity effect calculation. The proximity effect is calculated similarly to the lateral inhibition, but in this case α is the angle to the closest field in the plan. The weight for the proximity effect calculation is adjusted with a parameter value. The amount of the proximity effect is then subtracted from the original values of the objective function to decrease the importance of fields located close to each other.

Minimum Field Separation Angle

The PGO can exclude fields located close to each other by using a limiting value for the angle between fields in the final field configuration. The value for the limiting angle can be controlled by a parameter value.

Initial Field Removal Effects

The values of the field removal effects calculated during the first iteration are preserved for further use. These values contain information about the geometry of the patient, which is not included in the following iterations. The retained initial field removal effect values are included in the subsequent iterations by adding their weighted values into the current values of the objective function. The weight given to the initial field removal effects can be adjusted with a parameter value.

Local Optimization Mode for Plan Geometry

The local optimization continues from the result of the global optimization by fine-tuning parameters controlling the couch angles (for non-coplanar field geometry) and gantry angles (for both coplanar and non-coplanar field geometries). The collimator angles are also calculated if the limiting value for the collimator angle separation between adjacent fields is larger than zero. The local optimization does not change the number of fields in the plan, but it can test any couch and gantry angle combinations to find the optimal geometry. The progress of the local optimization is shown with the objective function curve and the *Number of iterations* parameter.

The local optimization can be performed in two modes that are defined as a calculation option for optimization: the Downhill Simplex method and the Powell method[39]. In addition to the mode, the maximum number of local optimization iterations is controlled with a calculation option.

The information about the best field configuration found is stored throughout the local optimization to make it always available if the local optimization is interrupted.

The local optimization can also be run alone without first running the global optimization. This might be useful for testing purposes. However, the best beam angle optimization results are achieved by running both global and local optimizations.

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[39] Information about the optimization methods: Numerical Recipes in C: The Art of Scientific Computing (William H. Press, et al.)

Note: *The Simplex and the Powell methods require the objective function evaluations only, not the derivatives.*

Number of IMRT Iterations in Objective Function Evaluations

The number of fluence optimization iterations to be run within the local optimization iteration can be controlled with a parameter value.

Initialization Phase

Initialization Phase in the Simplex Algorithm

In the initialization phase of the Simplex algorithm, the corner points of the original simplex are generated. The number of the corner points is N + 1, where N is the number of parameters to be optimized, that is, the gantry angles in the 2D case, and the gantry and couch angles in the 3D case. The generation of each corner point requires a calculation of the objective function. The distance from each corner point to the starting point (the amount of change applied to each parameter in the construction phase of the simplex) is controlled by a parameter value. This value is common for gantry and couch angles.

Initialization Phase in the Powell Algorithm

The Powell algorithm calculates line minimizations along the specified search directions. The search directions are initialized with unit vectors. Thus, in the first Powell iteration, each parameter is optimized separately. The initial step size is controlled with the same parameter value as is used for the Simplex algorithm. The search space for each parameter is expanded until there is a minimum point found between the line end points.

Optimization Phase

Optimization Phase in the Simplex Algorithm

After the construction of the original Simplex, the corner points are modified according to the algorithm schema. New corner points are found in Simplex iterations. At the beginning of a Simplex iteration, the stopping criteria for the algorithm are checked. If none of the criteria are met, the algorithm continues by finding a new position for the worst corner point in the Simplex. If there is no improvement found in the value of the objective function, the Simplex stops.

Optimization Phase in the Powell Algorithm

After initializing the search directions with unit vectors, the Powell proceeds according to the algorithm schema by finding the conjugate search directions. The calculations performed during the line minimizations along the current search directions are called Powell iterations. At the beginning of a Powell iteration, the stopping criteria for the algorithm are checked first.

Additional Stopping Criteria

In addition to the conditions in the optimization phase, the local optimization uses the following three additional stopping criteria.

Number of Objective Function Calculations

The maximum number of objective function calculations, that is, the number of local optimization iterations, can be used as a stopping criterion in the local optimization mode. This parameter is included in the list of input parameters for the PGO. However, it is not recommended to define a low value for this parameter, because the algorithm may not have reached a minimum point if the execution is stopped too early.

> **Note:** *In the Powell algorithm, the number of the calculated local optimization iterations is checked only at the beginning of a Powell iteration, not during the iteration. Therefore, the total number of local optimization iterations may exceed the given input parameter value.*

Convergence of the Algorithm

The convergence of the algorithm stopping criterion is used only for the Simplex algorithm.

The convergence of the algorithm is checked at the beginning of a Simplex iteration. If no significant changes are detected in the value of the objective function during recent iterations, the Simplex algorithm is stopped.

The evaluation of the convergence is controlled by the following parameter values:
- Number of Simplex iterations which is included in the evaluation.
- Limit value for the amount of change in the value of the objective function, which determines whether the optimization is continued.

These parameters are not PGO input parameters.

Invalid Field Parameters

Depending on the properties of the patient geometry and/or the definition of the valid gantry and couch angles, valid field parameters may not be found when generating new field directions in the local optimization. If valid field parameters cannot be found after a certain number of trials, the local optimization is stopped.

Progressive Resolution Optimizer (PRO) Algorithm

The Progressive Resolution Optimizer (PRO) algorithm creates VMAT (RapidArc) plans based on dose-volume objectives. VMAT fields use DMLC, variable dose rate and variable gantry speeds.

The PRO algorithm generates a sequence of control points which define MLC leaf positions and MU/deg as a function of gantry angle. MU/deg is encoded in DICOM and the Varian system database with the cumulative meterset weight, which defines the increase in MU between control points relative to the total MU in the field. This information is transferred to the treatment machine as such, and the machine control system determines how dose rate and gantry speed will be modulated to deliver the plan. After dose is calculated, Eclipse shows estimated dose rate and gantry speed values in the Field Properties and MLC Properties pages. These values are estimates, and they are not part of the information sent to the treatment machine.

The PRO algorithm uses an objective function to optimize the plan and to evaluate its quality. The objective function is the sum of the dose-volume and other user-defined objectives.

Progressive Resolution

The initial conditions for the PRO algorithm are defined using control points to represent each VMAT field. The algorithm uses multi-resolution approach (first described in the research on volumetric modulated arc therapy[40]) to optimize the plan. This means that the dose is modeled using first a lower number of dose calculation segments that are distributed evenly in each field. The number of dose calculation segments increases when moving from one multi-resolution level to another.

The dose in a dose calculation segment is calculated from the combined fluence through the MLC apertures at the control points located within a certain sector of the arc. Leaf motion is modeled by interpolating leaf positions between the control points. Leaf tongues are modeled by modifying the MLC aperture outline to effectively account for the tongue-and-groove effect.

The angle resolution of the dose calculation segments gets more accurate as the optimization progresses, and in consequence, the dose also gets more accurate. The number of control points remains the same during the whole optimization.

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[40] Otto, K: Volumetric Modulated Arc Therapy: IMRT in a Single Arc, Medical Physics, Vol. 35, no. 1, 2008, 310–317.

At the beginning of the optimization, the initial MLC shapes are conformed to the targets and the initial dose rates are equal for all dose calculation segments. The MLC shapes and dose rates of the different control points in the VMAT field are optimized. During the initial phases of the optimization bigger adjustments are made in leaf sequencing. The size of these adjustments decreases as the optimization progresses through the levels.

During the optimization, the algorithm proceeds through multi-resolution levels progressively increasing the accuracy of the dose calculation. At the first multi-resolution level, only a few dose calculation segments are used to model the dose, and each multi-resolution level contains progressively more dose calculation segments. The angle between the resulting dose calculation segments on the last multi-resolution level (4) will be approximately 2°-4°.The total number of dose calculation segments used depends on the span of the arc.

Inside each multi-resolution level there are several steps. Each step has its own internal calculation parameter set. The optimization allows some discontinuities in the delivery during early phases of the optimization, and decreases the size of the discontinuities stepwise as the optimization progresses. At the step borders, the delivery is forced to be within specified discontinuity levels. This may increase the objective function values when moving from one step to the next, and a peak in the objective function curve may be seen. The number of steps in different multi-resolution levels varies. Due to the nature of the optimization process, the PRO algorithm is not fully deterministic. Therefore successive optimizations with the same constraints may yield different results.

Avoidance Sectors

Avoidance sectors are ranges of gantry rotation with a zero delivered dose rate. You can define up to two avoidance sectors for each arc field in the optimization. The minimum length for an avoidance sector is 15 degrees. Similarly, the minimum length for the beam-on sector between two avoidance sectors, or between gantry start/stop angles and an avoidance sector is 15 degrees.

Avoidance sectors are supported only for Varian treatment units.

Mean Dose Objective

Mean dose objective is used to define the mean dose that should not be exceeded for a structure. It defines the mean dose in grays, but does not define any percentage of the structure that should not receive more than this dose. Mean dose objective is visualized in DVH during optimization, and it can be adjusted interactively during optimization. You can add one mean dose objective per structure. Mean dose objective cannot be used to increase the dose to a structure.

Jaw Tracking

Jaw tracking dynamically moves the collimator jaws during beam-on to keep them as close to the target projection as possible. This reduces leakage between the MLC leaves. The initial user-defined collimator jaw positions for the plan are used as the maximum limit for the jaws. Jaw tracking does not move the collimator jaws outside this maximum limit.

Note: *Not all VMAT-capable Varian linear accelerators support jaw tracking. The option can be selected in VMAT Optimization dialog box only for plans to be delivered with a treatment machine that supports jaw tracking. Jaw tracking is automatically on for Elekta MLCi and MLCi2.*

For PRO, the collimator speed in jaw tracking is set by defining the maximum speed value for Field X in a treatment unit operation limits in RT Administration.

Intermediate Dose

With the PRO algorithm you can optimize the plan, calculate the dose, and then use the calculated dose as an intermediate dose when continuing the optimization. This can be done manually by restarting the optimization and selecting "Use current plan dose as an intermediate dose for optimization" or automatically by selecting "Automatic intermediate dose" in the VMAT optimization dialog box when optimizing for the first time. This is useful especially if the DVH calculated during arc optimization deviates from the DVH produced during dose calculation, for example when there is a lot of heterogeneity in the volume to be treated.

The optimization algorithm can adjust the leaf sequences based on the intermediate dose. It calculates the error between the first round optimization result and the dose calculation, and during the second optimization round, when the optimization is finalized, it compensates for the differences and tries to achieve a better agreement. The second optimization round starts at the last multi-resolution level (level 4).

Restarting Optimization

Optimization can be restarted from user-defined arc fields. The user-defined fields may be produced, for example, in a previous arc optimization, or they may be created manually.

Before restarting the optimization, the algorithm re-samples the arc treatment to suitable control point spacing. The optimization restarts from the last multi-resolution level that has the most accurate dose modeling. To allow bigger adjustments to the leaf sequence, the user should rewind the multi-resolution levels. This will allow more flexibility in changing the leaf sequence. However, the dose on the earlier multi-resolution levels, calculated with the MRDC algorithm, is less accurate.

If the arc field does not contain a DMLC, optimization is restarted from the first resolution level, and the DMLC is not taken into account in the optimization.

Calculation Options for the PRO Algorithm

The PRO algorithm has the following calculation options:

- Inhomogeneity correction: Defines whether tissue heterogeneity correction is applied during optimization.
- Air cavity correction: An additional parameter for fine-tuning inhomogeneity correction. This parameter has no effect if the Inhomogeneity correction parameter is set to Off. When the air cavity correction option is used, the dose in an air cavity is smaller than without this option. On the other hand, the target/any part of the target should not be contoured in air, as the target will not get enough dose.

System Configuration for Dose Optimization

Note: *When configuring dose optimization algorithms, note the following:*

- *It is important to configure the system so that it corresponds to the characteristics of the treatment machine.*
- *Periodically perform follow-up measurements and compare with the dosimetric beam data used for configuring the beam. If fluctuations are large and the configured beam data no longer represents the average beam delivered by the machine, reconfigure the beam data using the newer dosimetric beam data.*
- *Measure all dosimetric beam data in as stable conditions as possible.*
- *Use the same file naming conventions in beam data measurements (input files) and in Beam Configuration (Therapy Unit name), and name the input files so that it is easy to match the beam data to the treatment unit during the configuration process.*

Beam Data Measurements for Dose Optimization

The configuration of the PO, DVO, PRO and PGO algorithms requires the same basic measured beam data as the calculation algorithms used for the dose calculation.

The following basic measured beam data is required for the configuration of all three optimization algorithms:

- Open field profiles (OPP) for several field sizes at five depths. The minimum number of measured profiles required is three, but using five is recommended.
- Open field diagonal profile (DPR) for largest field size at five depths. It is possible to configure PO, DVO, PRO and PGO algorithms without diagonal profiles. However, using diagonal profiles may improve the accuracy. It is recommended to use five measured diagonal profiles.
- Open field depth dose curves (OPD) for same field sizes as profiles.
- Source-phantom distance (SPD) in cm.
- Calculation grid size in cm. The calculation grid size used by MRDC dose calculation during optimization. For PO, DVO and PGO, the calculation grid size is fixed to 0.25 cm. The default calculation grid size for PRO is 0.25 cm. When configuring PRO for Elekta Beam Modulator, the grid size of 0.20 cm must be used.
- Nominal energy (In MRDC, the nominal energy is a parameter related to the maximum energy in MV of the photon spectra. The configuration program further modifies the photon spectra together with other configuration parameters so that the calculated dose matches with the measurements.)
- Profile measurement depths in cm.

Note: *The source-to-phantom distance (SPD) must be the same in the configuration of the dose calculation algorithm and the configuration of the PO, DVO and PRO algorithms. The SPD value is defined in the General Parameters in Beam Configuration.*

The PO, DVO, PRO and PGO have some special beam data configuration requirements:

- The maximum field sizes must be defined in the General Parameters (for instance, a 40×40 cm^2 field)
- Due to the characteristics of the optimization algorithm, the nominal energy (defined in the General Parameters) may not exceed 30 MV.

Detailed description of the measured depth dose curves and the measured profile curve field sizes: Configuration of Photon Beams on page 45.

Based on the measured beam data, the configuration produces the Model Parameters for the MRDC and an indicator parameter (Maximum Error for Dose Estimation) for the successfulness of the configuration. The parameter is the maximum gamma index with the criteria of 1% for dose difference and 1 mm for the distance to agreement. (Typically, the value for a successful configuration should be smaller than 5. If the value is higher, the reason could lie in the measured beam data). For PO and PRO, the configuration also produces a parameter (Scaler for Absolute Dose Calculation) that informs how the internal reference geometry is scaled to the absolute dose geometry.

Model Parameters for the Progressive Resolution Optimizer (PRO)

The table lists the parameters that need to be defined in Beam Configuration for the configuration of the PRO algorithm.

Table 34   Absolute Dose Calibration Parameters for PRO

Parameter	Description
Absolute dose reference field size [mm]	Size of the reference field used in configuration, expressed in millimeters. Usually, this should be the same size that was used to normalize the measured output factor table (that is, the field size for which the output factor = 1.0).
Absolute dose calibration source-phantom distance	Distance between the source and the surface of the phantom (SPD) used in configuration, expressed in millimeters. (Illustration of the geometry: Absolute Dosimetry Geometry on page 86.)
Absolute dose calibration depth [mm]	Depth of the reference point used in configuration, expressed in millimeters. (Illustration of the geometry: Absolute Dosimetry Geometry on page 86.)
Reference dose at calibration depth [Gy]	Absolute dose in water for the reference field size at the reference point at the calibration depth, expressed in Gray.
Reference MU at calibration depth [MU]	MU given to produce the reference dose for calibration.

Configuration of PO in Beam Configuration

You can configure the PO algorithm based on:

- Previously configured beam data for a dose calculation algorithm (AAA/Acuros XB).
- Previously configured beam data for a photon optimization algorithm (PRO/DVO/PGO). Instructions on copying the beam data from another calculation model: Beam Configuration Reference Guide.
- Basic measured beam data.

> **Note:** *The recommended procedure is to first configure the dose calculation algorithm (AAA/Acuros XB), and then configure the PO based on that.*

More details on using Beam Configuration: *Beam Configuration Reference Guide.*

Configure PO based on Configured AAA/Acuros XB

1. Go to Beam Configuration.
2. To add a calculation model for the PO algorithm if not available, choose **Beam Data** > **Configure Calculation Models** and add the model.
3. Verify that the dose calculation model you want to use (AAA/Acuros XB) is correctly configured in the system.
4. In the Scope window, select the optimization model to configure.
5. Choose **Insert** > **New Beam Data**.
6. Select the **Copy existing calculation model data to the optimization model** option.
7. Select the configured calculation model to use for the configuration of the new optimization model.
8. Click **OK**.
9. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. More information on the grid size: Beam Data Measurements for Dose Optimization on page 208.
10. In the Focus window, select the Open Field add-on and choose **Beam Data** > **Calculate Beam Data**.
11. If prompted to do so, select the beam data to be generated and click **OK** to start the calculation.
12. If the configuration was successful, approve the data.

Configure PO based on Configured PRO

1. Go to Beam Configuration.
2. To add a calculation model for the PO algorithm if not available, choose **Beam Data** > **Configure Calculation Models** and add the model.
3. In the Scope window, select the PO calculation model and choose **Insert** > **New Beam Data**.
4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.
5. Choose **File** > **Import** > **Eclipse Beam Data**, browse to the location of the appropriate beam data and import the data.
6. Match and assign the open field add-on.
7. In the Focus window, select Open Field, then choose **Insert** > **New Absolute Dose Calibration Parameters**, and type the same values to the parameters as are used in the AAA/Acuros XB configuration.

   The parameter values must be the same as in the AAA/Acuros XB configuration.

8. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. More information on the grid size: Beam Data Measurements for Dose Optimization on page 208.

9. In the Focus window, select the Open Field add-on and choose **Beam Data** > **Calculate Beam Data**.

10. If the configuration was successful, approve the data.

Configure PO based on Measured Beam Data

1. Go to Beam Configuration.

2. To add a calculation model for the PO algorithm if not available, choose **Beam Data** > **Configure Calculation Models** and add the model.

3. In the Scope window, select the PO calculation model and choose **Insert** > **New Beam Data**.

4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.

5. Absolute Dose Calibration Parameters default values are added.

6. Type the same values to the Absolute Dosimetry Calibration Parameters as are used in the AAA/Acuros XB configuration.

   The parameter values must be the same as in the AAA/Acuros XB configuration.

7. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. More information on the grid size: Beam Data Measurements for Dose Optimization on page 208.

8. To add the open field add-on, choose **Insert** > **New Add-On**.

9. To import the beam data in the w2CAD format, go to the Focus window, select Open Field, choose **File** > **Import** > **Measured Diagonal Profiles**, **Measured Depth Doses**, or **Measured Profiles**, depending on the measurement type, and navigate to the location of your measured beam data files.

10. In the Focus window, select the Open Field add-on and choose **Beam Data** > **Calculate Beam Data**.

11. If the configuration was successful, approve the data.

Configuration of DVO in Beam Configuration

You can configure the DVO algorithm based on:

- Previously configured beam data for a dose calculation algorithm (AAA/Acuros XB).
- Previously configured beam data for a photon optimization algorithm (PRO/DVO/PGO). Instructions on copying the beam data from another calculation model: Beam Configuration Reference Guide.
- Basic measured beam data.

Note: *The recommended procedure is to first configure the PRO algorithm (if available), and then configure the DVO based on that. If the PRO algorithm is not available, it is recommended to configure the DVO based on a dose calculation algorithm (AAA/Acuros XB).*

More details on using Beam Configuration: *Beam Configuration Reference Guide.*

Configure DVO based on Configured AAA/Acuros XB

1. Verify that the dose calculation model you want to use (AAA/Acuros XB) is correctly configured in the system.
2. In the Scope window, select the optimization model to configure.
3. Choose **Insert** > **New Beam Data.**
4. Select the **Copy existing calculation model data to the optimization model** option.
5. Select the configured calculation model to use for the configuration of the new optimization model.
6. Click **OK.**
7. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. More information on the grid size: Beam Data Measurements for Dose Optimization on page 208.
8. In the Focus window, select the Open Field add-on and choose **Beam Data** > **Calculate Beam Data.**
9. If prompted to do so, select the beam data to be generated and then click OK to start the calculation.

Configure DVO based on Configured PRO/DVO/PGO

1. Go to Beam Configuration.
2. To add a calculation model for the DVO algorithm if not available, choose **Beam Data** > **Configure Calculation Models** and add the model.
3. In the Scope window, select the DVO calculation model and choose **Insert** > **New Beam Data.**
4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.
5. Choose **File** > **Import** > **Eclipse Beam Data**, browse to the location of the appropriate beam data and import the data.
6. Match and assign the open field add-on.
7. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. More information on the grid size: Beam Data Measurements for Dose Optimization on page 208.
8. In the Focus window, select the Open Field add-on and choose **Beam Data** > **Calculate Beam Data.**

9. If the configuration was successful, approve the data.

Configure DVO based on Measured Beam Data

1. Go to Beam Configuration.
2. To add a calculation model for the DVO algorithm if not available, choose **Beam Data > Configure Calculation Models** and add the model.
3. In the Scope window, select the DVO calculation model and choose **Insert > New Beam Data**.
4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.
5. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. More information on the grid size: Beam Data Measurements for Dose Optimization on page 208.
6. To add the open field add-on, choose**Insert > New Add-On**.
7. To import the beam data in the w2CAD format, go to the Focus window, select Open Field, choose **File > Import > Measured Diagonal Profiles**, **Measured Depth Doses**, or **Measured Profiles**, depending on the measurement type, and navigate to the location of your measured beam data files.
8. In the Focus window, select the Open Field add-on and choose **Beam Data > Calculate Beam Data**.
9. If the configuration was successful, approve the data.

Configuration of PRO in Beam Configuration

You can configure the PRO algorithm based on:

- Previously configured beam data for a dose calculation algorithm (AAA/Acuros XB).
- Previously configured beam data for a photon optimization algorithm (PRO/DVO/PGO). Instructions on copying the beam data from another calculation model: Beam Configuration Reference Guide.
- Basic measured beam data.

> **Note:** *The recommended procedure is to first configure the dose calculation algorithm (AAA/Acuros XB), and then configure the PRO based on that.*

More details on using Beam Configuration: *Beam Configuration Reference Guide.*

Configure PRO based on Configured AAA/Acuros XB

1. Verify that the dose calculation model you want to use (AAA/Acuros XB) is correctly configured in the system.
2. In the Scope window, select the optimization model to configure.
3. Choose **Insert** > **New Beam Data**.
4. Select the **Copy existing calculation model data to the optimization model** option.
5. Select the configured calculation model to use for the configuration of the new optimization model.
6. Click **OK**.
7. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. More information on the grid size: Beam Data Measurements for Dose Optimization on page 208.
8. In the Focus window, select the Open Field add-on and choose **Beam Data** > **Calculate Beam Data**.
9. If prompted to do so, select the beam data to be generated and click **OK** to start the calculation.

Configure PRO based on Configured PRO/DVO/PGO

1. Go to Beam Configuration.
2. To add a calculation model for the PRO algorithm if not available, choose **Beam Data** > **Configure Calculation Models** and add the model.
3. In the Scope window, select the PRO calculation model and choose **Insert** > **New Beam Data**.
4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.
5. Choose **File** > **Import** > **Eclipse Beam Data**, browse to the location of the appropriate beam data and import the data.
6. Match and assign the open field add-on.
7. In the Focus window, select Open Field, then choose **Insert** > **New Absolute Dose Calibration Parameters**, and type the same values to the parameters as are used in the AAA/Acuros XB configuration.

   The parameter values must be the same as in the AAA/Acuros XB configuration.
8. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. More information on the grid size: Beam Data Measurements for Dose Optimization on page 208.
9. In the Focus window, select the Open Field add-on and choose **Beam Data** > **Calculate Beam Data**.

10. If the configuration was successful, approve the data.

Configure PRO based on Measured Beam Data

1. Go to Beam Configuration.
2. To add a calculation model for the PRO algorithm if not available, choose **Beam Data** > **Configure Calculation Models** and add the model.
3. In the Scope window, select the PRO calculation model and choose **Insert** > **New Beam Data**.
4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.
5. Absolute Dose Calibration Parameters default values are added.
6. Type the same values to the Absolute Dosimetry Calibration Parameters as are used in the AAA/Acuros XB configuration.

   The parameter values must be the same as in the AAA/Acuros XB configuration.
7. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. More information on the grid size: Beam Data Measurements for Dose Optimization on page 208.
8. To add the open field add-on, choose **Insert** > **New Add-On**.
9. To import the beam data in the w2CAD format, go to the Focus window, select Open Field, choose **File** > **Import** > **Measured Diagonal Profiles**, **Measured Depth Doses**, or **Measured Profiles**, depending on the measurement type, and navigate to the location of your measured beam data files.
10. In the Focus window, select the Open Field add-on and choose **Beam Data** > **Calculate Beam Data**.
11. If the configuration was successful, approve the data.

Configuration of PGO in Beam Configuration

The appropriate way of creating a PGO calculation model is to have it use the same beam data as the DVO calculation model. This is defined in the Add Calculation Model dialog box in Beam Configuration (choose **Beam Data** > **Configure Calculation Models**). It is not possible to assign existing beam data from another model to the PGO in the Insert New Beam Data dialog box. More information on Beam Configuration: *Beam Configuration Reference Guide*.

Input Parameters for PGO

The table lists the input parameters for the PGO algorithm used to control the execution. The table also includes information about the parameter types, their value ranges and default values (IEC 61217 for couch, gantry or collimator angles).

Table 35   Input Parameters for the PGO

Parameter name	Range (IEC 61217 for couch, gantry or collimator angles)	Default value (IEC 61217 for couch, gantry or collimator angles)	Use of Parameter
Initial field distribution	Coplanar, Non-coplanar, None	Coplanar	Information on the creation of the initial co-planar (2D) and non-coplanar (3D) field geometries: Initial Field Geometries on page 195. Selecting None skips the global optimization and uses the active plan in Eclipse as input for local optimization.
Initial number of fields	2–400	71	Defines the initial number of fields to be created for the global optimization. However, the field geometry is checked before running the global optimization for fields that enter the patient through the end(s) of the CT stack (these fields are excluded). The number of fields left in the initial field distribution after the check may be lower than the number specified by this parameter.
Minimum number of fields	2–15	5	Defines the lower limit for the number of fields to be left in the plan after global optimization.
Maximum number of fields	2–15	9	Defines the upper limit for the number of fields to be left in the plan after global optimization.

Parameter name	Range (IEC 61217 for couch, gantry or collimator angles)	Default value (IEC 61217 for couch, gantry or collimator angles)	Use of Parameter
Maximum collimator variation [deg]	0–180	0	Controls the variation of the collimator angle values between adjacent fields in the initial field distribution.
			0 = Leaves the collimators to zero angle (IEC 61217 scale, which corresponds to 180 degrees in the Varian Standard scale).
			180 degrees = The collimators are rotated between 270 degrees (that is, –90 degrees) and 90 degrees so that the direction of the MLC leaves coincides with the shortest dimension of the PTV in the BEV. This choice aims at the lowest possible number of carriage groups, and often also minimizes the exposure of healthy tissue.
			> 180 degrees = The collimator angles stay within the specified limit. The movement direction of the leaves coincides with the shortest dimension of the PTV.
			Individual machine limits for collimator angle rotation are not taken into account by the PGO. Constraining the collimator angle values to 270–90 degrees is considered sufficient for most linear accelerators.
Coplanar offset angle [deg]	0–90	0	Adjusts the offset to the starting gantry angle (default = 0 degrees in IEC 61217, which corresponds to 180 degrees in the Varian Standard scale) for coplanar initial field distribution. Does not affect the non-coplanar initial field distribution.
Maximum elevation angle for non-coplanar fields [deg]	0–90	90	Controls the maximum elevation from the coplanar plane for non-coplanar initial field distribution.
Fluence iterations per global geometric iteration	1–20	3	Defines the number of fluence optimization iterations to be run in the global optimization.

Parameter name	Range (IEC 61217 for couch, gantry or collimator angles)	Default value (IEC 61217 for couch, gantry or collimator angles)	Use of Parameter
Field reduction rate	0–1	0.5	Controls the number of fields to be removed from the plan during the global optimization. Increasing the value also increases the number of fields to be removed in each global geometry iteration, which makes the algorithm faster. However, it is not recommended to increase this value above 0.5.
Field number constraint weight	0–1	0.4	Controls the cost for leaving more fields in the final plan (Field Number Objective on page 199).
First global iteration weight	0–1	0.1	Description of the use of this parameter: Initial Field Removal Effects on page 202.
Lateral inhibition weight	0–1	0.4	Description of the use of this parameter: Lateral Inhibition on page 200.
Proximity effect weight	0–1	0.4	Description of the use of this parameter: Proximity Effect on page 201.
Minimum field separation angle [deg]	0–90	10	Controls how close to each other the fields are allowed to stay in the final plan after the global optimization. The parameter also applies to the local optimization.
Local geometric optimization mode	Simplex, Powell, None	Simplex	Defines the mode for the local optimization. Selecting None skips the local optimization.
Fluence iterations per local geometric iteration	1–20	3	Defines the number of fluence optimization iterations in the local optimization.
Maximum number of local optimization iterations	0–500	40	Defines the upper limit for the number of objective function evaluations to be calculated in the local optimization and controls the execution time of the local optimization (Local Optimization Mode for Plan Geometry on page 202).
Initial step size in local optimization [deg]	1–180	10	Defines the initial distance between the original and the new field direction in the local optimization. Used by Simplex and Powell optimization.